

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A synthetic or isolated nucleic acid fragment which comprises a nucleotide sequence that is identical or fully complementary to a first sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.
2. (Previously Presented) The nucleic acid fragment according to claim 1, wherein said nucleotide sequence is identical or fully complementary to a second sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.
- 3-4. (Canceled)
5. (Currently Amended) A probe for identifying *Trypanosoma cruzi*, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said probe contains at least ~~5~~ 7 and no more than 100 nucleotides.
6. (Canceled)
7. (Previously Presented) The probe according to claim 5, wherein said probe has 8 to 50 nucleotides.
8. (Currently Amended) A primer for amplifying a nucleotide sequence, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said primer contains at least ~~5~~ 7 and no more than 30 nucleotides.

9. (Canceled)

10. (Previously Presented) The primer according to claim 8, wherein said primer consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:12.

11. (Previously Presented) A reagent for detecting or identifying *Trypanosoma cruzi* in a biological sample, said reagent comprising a capture probe and a detection probe, both in accordance with claim 5, wherein said capture probe and said detection probe have nucleotide sequences that are different from one another.

12. (Original) The reagent according to claim 11, wherein said capture probe is attached to a solid support.

13. (Original) The reagent according to claim 12, wherein said capture probe is directly attached to said solid support.

14. (Original) The reagent according to claim 12, wherein said capture probe is indirectly attached to said solid support.

15. (Original) The reagent according to claim 11, wherein said detection probe is labeled by a marker selected from the group consisting of radioactive isotopes, enzymes capable of hydrolyzing a chromogenic, fluorogenic or luminescent substrate, chromophoric chemical compounds, fluorogenic compounds, luminescent compounds, nucleotide base analogs, and biotin.

16. (Original) The reagent according to claim 15, wherein said enzymes are selected from the group consisting of peroxidase and alkaline phosphatase.

17. (Previously Presented) The reagent according to claim 11, further comprising at least one primer consisting essentially of a segment of at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting at

nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

18. (Previously Presented) A method for detection and/or identification of *Trypanosoma cruzi* in a biological sample, comprising exposing denatured DNA extracted from *Trypanosoma cruzi* or DNA obtained by reverse transcription of RNA extracted from *Trypanosoma cruzi* to at least one probe according to claim 5; and detecting hybridization of said probe.

19. (Original) A method for detection and/or identification of *Trypanosoma cruzi* in a biological sample, comprising exposing extracted RNA from *Trypanosoma cruzi* to at least one probe according to claim 5; hybridizing said probe with said RNA; and detecting said hybridization.

20. (Previously Presented) The method according to claim 18, wherein before said DNA is exposed to said probe, said DNA is amplified in the presence of an enzymatic system with at least one primer, wherein said primer consists essentially of a segment of at least five contiguous nucleotides of a nucleic acid sequence that is identical or fully complementary to a sequence identified in SEQ ID NO: 1 or the corresponding RNA sequence.

21. (Previously Presented) A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

22. (Previously Presented) A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence

that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

23. (Previously Presented) A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

24. (Previously Presented) The nucleic acid fragment of claim 23, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

25. (Previously Presented) A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

26. (Previously Presented) A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

27. (Previously Presented) A process for detecting and/or identifying *Trypanosoma cruzi* in a biological sample, comprising:

exposing DNA or RNA from the sample to a probe under such conditions that said probe hybridizes to a nucleotide sequence identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence; and

detecting hybridization of the probe to said DNA or RNA to detect and/or identify Trypanosoma cruzi.

28-31. (Canceled)

32. (Previously Presented) The reagent of claim 17, wherein said primer contains no more than 30 nucleotides.

33. (Canceled)

34. (Previously Presented) The method of claim 20, wherein said primer contains no more than 30 nucleotides.

35. (Canceled)

36. (Previously Presented) The nucleic acid fragment of claim 21, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

37. (Previously Presented) The nucleic acid fragment of claim 22, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

38. (Previously Presented) The nucleic acid fragment of claim 23, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

39. (Previously Presented) The probe of claim 5, wherein said probe contains at least five contiguous nucleotides of said nucleotide sequence.

40. (Previously Presented) The primer of claim 8, wherein said primer contains at least five contiguous nucleotides of said nucleotide sequence.

41-42. (Canceled)

43. (New) The probe according to claim 5, wherein said probe has 8 to 100 nucleotides.

44. (New) The primer according to claim 8, wherein said primer has 8 to 30 nucleotides.

45. (New) A probe for identifying *Trypanosoma cruzi*, consisting essentially of a nucleic acid having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said nucleic acid contains at least 5 and no more than 100 nucleotides, and wherein said nucleic acid is isolated from nucleic acids that do not have at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

46. (New) A primer for amplifying a *Trypanosoma cruzi* nucleotide sequence, consisting essentially of a nucleic acid having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at

nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said nucleic acid contains at least 5 and no more than 30 nucleotides, and wherein said nucleic acid is isolated from nucleic acids that do not have at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.